

## OBD & PHENOTE: TOOLS FOR STORAGE AND ANNOTATION OF BIOMEDICAL DATA USING ONTOLOGIES

Washington, N.; Mungall, C.; Shu, SQ.; Gibson, M.; Day-Richter, J.; Misra, S.; Lewis, S.  
Life Sciences Division, Lawrence Berkeley National Labs, Berkeley, CA

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Today's rapidly increasing amount of sequenced genomes allows for more cross-species comparisons of genes and gene-products than ever before. Current automated investigation of genomes is limited to simple queries of sequence and feature data, and any cross-species relationships based on phenotype and functional data must be accomplished by human intervention. The next generation of intelligent bioinformatics tools that will computationally identify new cross-species functional relationships between genes, mutant phenotypes, and human diseases requires resources for storage and access of experimental data that is annotated in a standardized format.

The **Open Biomedical Database (OBD)** created by the National Center for Biomedical Ontology is a centralized resource for life scientists, clinicians, and bioinformaticists to store and analyze ontology-based annotations linked to primary experimental data. Standardized annotations of experimental data using phenotype and other ontologies will enable researchers to make sophisticated multiple-species queries related to phenotypes and diseases. OBD will accommodate a wide variety of experimental data, and its development is being driven by our collaborating Driving Biological Projects. Current types of data stored in OBD include mutant phenotypes with their associated genotypes in model organisms, disease state information derived from Online Mendelian Inheritance in Man (OMIM), and meta-data associated with clinical trials. The experimental data is stored and queried as triples (entity, attribute, value) described by ontology terms found in the Core 1 **Open Biomedical Ontologies (OBO)**. We have developed a software tool called **Phenote** to facilitate annotation of phenotype data in both stand-alone and web-based formats. Future improvements include integration of the OBD query and browser functions into **BioPortal** to deliver experimental results in a researcher-friendly format.

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E-mail: NLWashington@lbl.gov